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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds  
(without alignments)  
777.677 Million cell updates/sec

Title: U5-09-296-264-9

Perfect score: 20

Sequence: 1 tgaagtcgcggcgcgaagtcgc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21:\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	AAZ31439 Human neu
2	20	100.0	20	9	ADA74691 GTI3609 a
3	15.8	79.0	23	10	ABZ26016 Orthosomy
4	15.2	76.0	60	6	ABR49870 Human bpl
5	15.2	76.0	100	8	ACD79788 E. coli K
6	15	75.0	24	2	AAV55815 Multimeri
7	15	75.0	24	2	AAV55817 Multimeri
8	14.8	74.0	25	9	ACI45513 Human mlc
9	14.8	74.0	48	2	AAQ28729 Sequence
10	14.8	74.0	48	2	AAQ28730 Sequence
11	14.4	72.0	25	9	ACI86896 Human mlc
12	14.4	72.0	25	9	ACH59512 DNA large
13	14.4	72.0	60	6	ABN48299 Human bpl
14	14.2	71.0	20	12	ADJ23951 Human end
15	14.2	71.0	20	12	ADJ23488 Human end
16	14.2	71.0	21	2	AAQ70342 Antisense
17	14.2	71.0	24	10	ABZ58545 PCR prime
18	14.2	71.0	30	2	AAQ31897 PCR prime
19	14.2	71.0	30	3	AAA95218 G+C rich

C	20	14.2	71.0	30	10	ADC66453	Adc66453 Human Fra
	21	14.2	71.0	50	2	AAx52367	AAx52367 Probe use
	22	14.2	71.0	50	3	ADC78471	ADC78471 Human PRO
	23	14.2	71.0	50	4	AAf72525	AAf72525 Human PRO
C	24	14.2	71.0	50	4	AAI33769	AAI33769 Human SNP
	25	14.2	71.0	50	4	AAI33771	AAI33771 Human SNP
C	26	14.2	71.0	50	4	AAI33772	AAI33772 Human SNP
	27	14.2	71.0	50	8	ACA60124	ACA60124 Human sec
	28	14.2	71.0	50	8	ACD07524	ACD07524 Novel hum
	29	14.2	71.0	50	8	ABX71572	ABX71572 Human sec
	30	14.2	71.0	50	8	ACH06904	ACH06904 Human sec
	31	14.2	71.0	50	8	ABX96141	ABX96141 Human sec
	32	14.2	71.0	50	8	ACA05462	ACA05462 Human sec
	33	14.2	71.0	50	8	ACD20129	ACD20129 Human sec
	34	14.2	71.0	50	8	ACA54932	ACA54932 Novel sec
	35	14.2	71.0	50	9	ACD19767	ACD19767 Human sec
	36	14.2	71.0	50	9	ADB29356	ADB29356 Human sec
	37	14.2	71.0	50	9	ADA18212	ADA18212 Human sec
	38	14.2	71.0	50	9	ACD66914	ACD66914 Human sec
	39	14.2	71.0	50	9	ACD83075	ACD83075 Human PRO
	40	14.2	71.0	50	9	ADA16187	ADA16187 Human sec
	41	14.2	71.0	50	9	ADA42332	ADA42332 Human sec
	42	14.2	71.0	50	9	ACD23253	ACD23253 Human PRO
	43	14.2	71.0	50	9	ADA16611	ADA16611 Human sec
	44	14.2	71.0	50	9	ADA13040	ADA13040 Human sec
	45	14.2	71.0	50	9	ADA41908	ADA41908 Human sec

ALIGNMENTS

RESULT 1  
AAZ31439  
ID AAZ31439 standard; DNA; 20 BP.

XX AAZ31439;  
XX  
XX  
DT 07-FEB-2000 (first entry)

DE Human neuropilin mRNA specific antisense oligo GTI3609.

XX Neuropilin, human; growth; metastasis; tumor; neovascularisation; cancer;

KW papilloma; diabetic retinopathy; antisense; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9955855-A2.

XX PD 04-NOV-1999.

XX PF 23-APR-1999; 99WO-CA000324.

XX PR 23-APR-1998; 98US-0082791P.

PA (GENE-) GENESENNSE TECHNOLOGIES INC.

PI Wright JA, Young AH, Lee YS;

DR WPI; 2000-023357/02.

PT Antisense oligonucleotides that inhibit neuropilin expression, useful for

PT treating cancer.

PS Claim 4; Page 16; 57BP; English.

Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit  
human neuropilin expression. The antisense oligonucleotides can be used  
to inhibit the growth or metastasis of a mammalian tumor and inhibit  
neovascularisation. The oligonucleotides may be used to treat various  
forms of cancers or tumors, such as sarcomas, melanomas, adenomas,  
carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of  
the mouth, throat, larynx and lung, genitourinary cancers such as

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast  
 CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver  
 CC cancer, head and neck cancers, and nervous system cancers, as well as  
 CC benign lesions such as papillomas. The methods may be used to treat  
 CC neovascularisation disorders such as diabetic retinopathy, and  
 CC retinopathy of prematurity and age related macular degeneration  
 XX  
 SQ Sequence 20 BP; 3 A; 2 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGGAAGTGC 20  
 |||||  
 1 TGAGTGGCGGTGGAAGTGC 20

RESULT 2  
 ADA74691

ID ADA74691 standard; DNA; 20 BP.

AC ADA74691;

XX 20-NOV-2003 (first entry)

DE GRI3609 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;  
 KM cytoskeletal; growth; tumour metastasis; angiogenesis; gene therapy;  
 KM GRI3609; antisense; human; ss.

XX Homo sapiens.

OS

PN US2003083274-A1.

XX 01-MAY-2003.

XX 22-APR-1999; 99US-00296264.

XX 23-APR-1998; 98US-0082791P.

XX (WRIG/) WRIGHT J A.

XX (YOUN/) YOUNG A H.

XX (LEEY/) LEE Y S.

XX Wright JA, Young AH, Lee YS;

XX WPI; 2003-576622/54.

XX New antisense oligonucleotide that inhibits neuropilin expression, useful  
 PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a  
 PT mammalian tumor.

XX Claim 1; Page 5; 27pp; English.

XX The invention relates to a novel antisense oligonucleotide that inhibits  
 CC the expression of neuropilin, also known as VEGF165R (vascular  
 CC endothelial growth factor receptor). The oligonucleotide of the invention  
 CC demonstrates cytostatic activity and may be useful for inhibiting the  
 CC growth or metastasis of a mammalian tumor and to inhibit angiogenesis in  
 CC mammals. Furthermore, the oligonucleotide may be utilised during gene  
 CC therapy. The current sequence is that of the GRI3609 antisense  
 CC oligonucleotide of the invention which is targeted to human neuropilin  
 CC mRNA.

XX Sequence 20 BP; 3 A; 2 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGGAAGTGC 20

Db 1 TGAGTGGCGGTGGAAGTGC 20  
 |||||

RESULT 3  
 AB226016/c  
 ID AB226016 standard; DNA; 23 BP.

XX AB226016;

XX 21-MAR-2003 (first entry)

DE Orthosomycin biosynthetic gene related oligonucleotide UEBR-S1.

XX Orthosomycin; biosynthesis; evernimycin; avilamycin; PCR; primer;  
 KM probe; ss.

XX Synthetic.

XX WO200279505-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-CA000432.

XX 28-MAR-2001; 2001US-0279095P.

XX 30-MAR-2001; 2001US-0279709P.

XX 20-APR-2001; 2001US-0285214P.

XX (ECOP-) ECOPRIA BIOSCIENCES INC.

XX Farnet CM, Zazopoulos E, Scaffa A;

XX WPI; 2003-058435/05.

XX Identifying orthosomycin biosynthetic gene, gene fragment or gene  
 PT cluster, by detecting presence of nucleic acid sequence corresponding to  
 PT 17 of flambamycins protein families.

XX Example 6; Page 109; 51pp; English.

XX The invention relates to identifying orthosomycin biosynthetic genes and  
 CC its fragment/gene cluster (AB26670-AB266813), comprising detecting the  
 CC presence of a nucleic acid sequence coding for a polypeptide (ABP99207-  
 CC ABP99362). The method is useful for identifying an orthosomycin  
 CC biosynthetic gene, gene fragment or gene cluster, especially an  
 CC evernimycin-type or avilamycin-type orthosomycin biosynthetic gene,  
 CC gene fragment or gene cluster. The method is useful for detecting the  
 CC presence of any organism that contains DNA for the production of  
 CC orthosomycins (both evernimycin-type orthosomycins and avilamycin-type  
 CC orthosomycins) regardless of the level at which genes for orthosomycin  
 CC production are expressed by the organism or the amount of orthosomycin  
 CC produced by the organism. This allows for the detection of new  
 CC orthosomycin natural products, not produced by the organism. The present  
 CC sequence is that of an oligonucleotide designed to be used as a PCR  
 CC primer or probe for identifying orthosomycin biosynthetic loci in other  
 CC organisms  
 XX

SQ Sequence 23 BP; 4 A; 11 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 10; Length 23;  
 Best Local Similarity 89.5%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAGGTGGCGGTGGAAGTGC 20  
 |||||  
 21 GAGTGGCGGTGGAAGTGC 3

Db 21 GAGTGGCGGTGGAAGTGC 3

RESULT 4  
 ABN49870  
 ID ABN49870 standard; DNA; 60 BP.

XX

AC	ABN99870;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Human spliced transcript detection oligonucleotide SEQ ID NO:22618.
XX	
KW	Human; mouse; rat; splice transcript; detection; RNA transcript;
KW	splice variant; transcriptome; oligonucleotide library; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200210449-A2.
XX	
PD	07-FEB-2002.
XX	
PF	20-JUL-2001; 2001WO-1B001903.
XX	
PR	28-JUL-2000; 2000US-0221607P.
XX	
PR	02-MAY-2001; 2001US-0287724P.
XX	
PA	(COMP-) COMPUGEN INC.
XX	
PI	Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX	
DR	WPI, 2002-257383/30.
XX	
PT	New oligonucleotide libraries comprising oligonucleotides which
PT	selectively hybridize to mRNAs transcribed from a transcription unit of a
PT	genome, useful for detecting tissue-, pathology-, and developmental-
PT	specific genes.
XX	
PS	Example 1; SEQ ID NO 22618; 47pp; English.
XX	
CC	The present invention describes oligonucleotide libraries for detecting
CC	messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC	)transcriptome comprises messenger RNAs transcribed from multiple
CC	transcription units that populate a genome. The library comprises several
CC	oligonucleotides, each capable of hybridizing selectively to a set of
CC	messenger RNAs transcribed from a given transcription unit of the genome,
CC	which encodes one or more messenger RNA splice variants. The
CC	oligonucleotide libraries are useful for detecting mRNAs from a
CC	biological sample, in expression profiling studies, in qualitatively or
CC	quantitatively characterizing the corresponding transcriptome, and in
CC	detecting RNA transcripts and splice variants of human or animal
CC	transcriptomes. The libraries may also be used as specialised mini
CC	libraries to detect transcripts of a sub-transcriptome under a particular
CC	biological or pathological state, and so allowing the detection of tissue
CC	- and pathology-specific genes such as those genes only expressed in
CC	specific tissue under a specific pathological condition; to detect
CC	variants of a specific gene; and to detect RNA transcripts and splice
CC	variants of a transcriptome of a patient suffering from a particular
CC	disorder. ABN97253 to ABN95989 represent oligonucleotide sequences from
CC	rats, humans and mice, which are used in the exemplification of the
CC	present invention. N.B. The sequence data for this patent did not form
CC	part of the printed specification, but was obtained in electronic format
CC	directly from WIPO at <a href="http://ftp.wipo.int/pub/published_pct_sequences">ftp.wipo.int/pub/published_pct_sequences</a>
XX	
SQ	Sequence 60 BP; 17 A; 12 C; 18 G; 13 T; 0 U; 0 Other;
XX	
Query Match	76.0%; Score 15.2; DB 6; Length 60;
Best Local Similarity	85.0%; Pred. No. 3.7e+03;
Matches 17; Conservative	0; Mismatches 3; Indels 0; Gaps 0
OY	1 TGAGGTGCGGTGGAAGTGC 20
DB	25 TGAGTGTCTGTGTGATGTCC 44
XX	
RESULT 5	
ID	ACD979788 standard; DNA; 100 BP.
XX	
AC	ACD979788;

```

XX 19-SEP-2003 (first entry)
XX
XX E. coli K12 MG1655 biochip probe SEQ ID 11064.
XX
XX Biochip: gene expression; gut; diagnostic; detection; probe; ss.
XX
XX Escherichia coli.
XX
XX EP1260592-A1.
XX
XX 27-NOV-2002.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX (MMGB-) MMGB-BIOTECH AG.
XX
XX Donner H, Drescher B, Huber A, Weber J;
XX
XX WPI, 2003-241155/24.
XX
XX Biochip containing probes complementary with open reading frames in
XX
XX Escherichia coli K12, useful for detecting gene expression and expression
XX
XX patterns.
XX
XX Claim 3; Page 1724; 2004JP; German.
XX
XX This invention describes a novel biochip comprising probe spots, each
XX
XX containing many identical probes. The probes are nucleotide sequences of
XX
XX 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
XX
XX least one includes a segment of at least 20 bases identical with, or
XX
XX complementary to, a segment of an open reading frame (orf) of Escherichia
XX
XX coli K12. The biochip is used for specific detection of gene expression
XX
XX in K12 and for determining the gene expression pattern, e.g. for
XX
XX diagnostic determination of which E. coli strains are present in the gut,
XX
XX and to determine the effects of e.g. growth media on gene expression. The
XX
XX biochip provides as comprehensive as possible detection of the K12
XX
XX genome, with simultaneous analysis of many different genes with a single
XX
XX device, and comparison of gene expression between K12 and its mutants or
XX
XX other E. coli strains in a single experiment. Apart from qualitative and
XX
XX quantitative information about gene expression, it also allows the use of
XX
XX measurements of population densities for the various strains. The use of
XX
XX synthetic oligonucleotides for preparation of probes allows free
XX
XX variation in probe length and ensures high purity (and thus selectivity,
XX
XX reactivity and reproducibility); also synthetic probes are generally
XX
XX shorter than probes prepared by polymerase chain reaction. ACD68731 to
XX
XX ACDB1540 represent oligonucleotide probes used with the biochip described
XX
XX in the invention
XX
XX
XX Sequence 100 BP; 28 A; 16 C; 30 G; 26 T; 0 U; 0 Other;
XX
XX
XX
XX
XX Query Match 76.0%; Score 15.2; DB 8; Length 100;
XX
XX Best Local Similarity 85.0%; Pred. No. 3.8e+03;
XX
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0
XX
XX
XX 1 TGAGGTGCGGTTGGAAGTGC 20
XX ||||| ||||| |||||
XX 31 TGAGGTGCGCGAGGAAATGC 50
XX
XX
XX
XX
XX RESULT 6
XX AAV55815/c
XX ID AAV55815 standard; DNA; 24 BP.
XX
XX AAV55815;
XX
XX
XX 27-AUG-2003 (revised)
XX
XX 18-NOV-1998 (first entry)
XX
XX
XX Multimerisation of minimal motifs using primer ZG62.
XX
XX

```

KM Fusion protein; stabilising polypeptide; proteolytic degradation;  
 KM resistance; half-life; autoimmune disease; inflammation; nitro drug;  
 KM Ikappab regulator protein; inflammatory bowel disease; in vivo imaging;  
 KM nitroreductase protein; enzyme therapy; produg therapy; protease;  
 KM cancer; pathological condition; minimal motif; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Human herpesvirus 4.  
 XX  
 PN MO9822577-A1.  
 XX  
 PD 28-MAY-1998.  
 XX  
 PD 17-NOV-1997; 97WO-IB001508.  
 XX  
 PF 15-NOV-1996; 96US-0030986P.  
 XX  
 PR 25-JUN-1997; 97US-0048945P.  
 XX  
 PA (MASU/) MASUCCI M G.  
 XX  
 PI Maucuci MG;  
 PI  
 DR WPI; 1998-312463/27.  
 XX  
 PT New fusion proteins resistant to proteolytic degradation - comprising a  
 PT core protein with a stabilising polypeptide comprising a peptide sequence  
 PT containing glycine repeats.  
 XX  
 PS Disclosure; Page 72; 120pp; English.  
 XX  
 CC Sequences shown in AAV55812 to AAV55827 represent primers used in the  
 CC course of the invention for the multimerisation of minimal motifs. The  
 CC invention provides a method for increasing the resistance of a core  
 CC protein to proteolytic degradation that comprises linking or inserting  
 CC onto or into the core protein a stabilising polypeptide of formula  
 CC [(Glya)(X)(Glyb)(Y)(Glyc)(Z)n where Glya, Glyb, Glyc are 1-6 sequential Gly  
 CC residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr  
 CC and n can be anything between 1-66. X, Y and Z need not be identical from  
 CC n repeat to n repeat. Alternatively a nucleic acid encoding a stabilising  
 CC polypeptide can be linked onto or inserted into a nucleic acid encoding a  
 CC core protein. The fusion proteins of the invention are more resistant to  
 CC degradation by proteases and, thus, have a longer half-life than the  
 CC unused core protein. The products can be used for treating autoimmune  
 CC diseases, cancer and inflammation. In particular, the core protein may be  
 CC an Ikappab regulator protein for the treatment of inflammatory bowel  
 CC disease, or a nitroreductase protein which can activate nitro drugs in  
 CC enzyme/produg therapy to treat cancer or other pathological conditions.  
 CC The fusion proteins can also be used in diagnostic methods such as in  
 CC vivo imaging. (Updated on 27-AUG-2003 to correct OS field.)  
 CC  
 XX  
 SQ Sequence 24 BP; 4 A; 14 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 75.0%; Score 15; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GAGGTGCGGGTGAA 16  
 |||||||||  
 Db 15 GAGGTGCGGGTGAA 1  
 |||||||||  
 RESULT 7  
 AAV55817/C  
 ID AAV55817 standard; DNA; 24 BP.  
 XX  
 AC AAV55817;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 18-NOV-1998 (first entry)  
 XX  
 DE Multimerisation of minimal motifs using primer ZGR2.  
 XX  
 KM Fusion protein; stabilising polypeptide; proteolytic degradation;

KM resistance; half-life; autoimmune disease; inflammation; nitro drug;  
 KM Ikappab regulator protein; inflammatory bowel disease; in vivo imaging;  
 KM nitroreductase protein; enzyme therapy; produg therapy; protease;  
 KM cancer; pathological condition; minimal motif; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Human herpesvirus 4.  
 XX  
 PN MO9822577-A1.  
 XX  
 PD 28-MAY-1998.  
 XX  
 PD 17-NOV-1997; 97WO-IB001508.  
 XX  
 PF 15-NOV-1996; 96US-0030986P.  
 XX  
 PR 25-JUN-1997; 97US-0048945P.  
 XX  
 PA (MASU/) MASUCCI M G.  
 XX  
 PI Maucuci MG;  
 PI  
 DR WPI; 1998-312463/27.  
 XX  
 PT New fusion proteins resistant to proteolytic degradation - comprising a  
 PT core protein with a stabilising polypeptide comprising a peptide sequence  
 PT containing glycine repeats.  
 XX  
 PS Disclosure; Page 72; 120pp; English.  
 XX  
 CC Sequences shown in AAV55812 to AAV55827 represent primers used in the  
 CC course of the invention for the multimerisation of minimal motifs. The  
 CC invention provides a method for increasing the resistance of a core  
 CC protein to proteolytic degradation that comprises linking or inserting  
 CC onto or into the core protein a stabilising polypeptide of formula  
 CC [(Glya)(X)(Glyb)(Y)(Glyc)(Z)n where Glya, Glyb, Glyc are 1-6 sequential Gly  
 CC residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr  
 CC and n can be anything between 1-66. X, Y and Z need not be identical from  
 CC n repeat to n repeat. Alternatively a nucleic acid encoding a stabilising  
 CC polypeptide can be linked onto or inserted into a nucleic acid encoding a  
 CC core protein. The fusion proteins of the invention are more resistant to  
 CC degradation by proteases and, thus, have a longer half-life than the  
 CC unused core protein. The products can be used for treating autoimmune  
 CC diseases, cancer and inflammation. In particular, the core protein may be  
 CC an Ikappab regulator protein for the treatment of inflammatory bowel  
 CC disease, or a nitroreductase protein which can activate nitro drugs in  
 CC enzyme/produg therapy to treat cancer or other pathological conditions.  
 CC The fusion proteins can also be used in diagnostic methods such as in  
 CC vivo imaging. (Updated on 27-AUG-2003 to correct OS field.)  
 CC  
 XX  
 SQ Sequence 24 BP; 3 A; 14 C; 2 G; 5 T; 0 U; 0 Other;  
 Query Match 75.0%; Score 15; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GAGGTGCGGGTGAA 16  
 |||||||||  
 Db 15 GAGGTGCGGGTGAA 1  
 |||||||||  
 RESULT 8  
 AC145513/C  
 ID AC145513 standard; DNA; 25 BP.  
 XX  
 AC AC145513;  
 XX  
 DT 13-OCT-2003 (first entry)  
 DE Human microarray DNA oligonucleotide SEQ ID NO 45504.  
 XX  
 KM EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KM genetic variation; diallelic marker; polymorphism; human;  
 KM cross-species comparison.

XX OS Homo sapiens.  
 XX PN US2003104410-A1.  
 XX PD 05-JUN-2003.  
 XX PF 15-MAR-2002; 2002US-00098263.  
 XX PR 16-MAR-2001; 2001US-0276759P.  
 XX PA (AEFY-) AEFYMETRIX INC.  
 XX PI Mitmann MP;  
 XX DR WPI; 2003-567953/53.  
 XX PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX PS Claim 1; SEQ.ID NO 45504; 9pp; English.  
 XX CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying diallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 XX SQ Sequence 25 BP; 7 A; 8 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 74.0%; Score 14.8; DB 9; Length 25;  
 Best Local Similarity 88.9%; Pred. No. 5.3e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TGAGTGGCGGTGGAAGT 18  
 Db 24 TGAGTTTCGCTCGAAGT 7  
 RESULT 9  
 AAQ28729 ID AAQ28729 standard; DNA; 48 BP.  
 XX AC AAQ28729;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 27-FEB-1993 (first entry)  
 XX DE Sequence of oligonucleotide 2119 corresponding to the linking peptide  
 XX between VH and VL domains of plasmid pFVCD3-H-gamma-3.  
 XX KW Chimeric polypeptide; cell surface CD4 molecule; HIV type 1; HIV-1;  
 KW human immunodeficiency virus; antigen binding site; cytotoxic T-; cell;  
 KW CD3 molecule; T-cell receptor complex; PCR; ss.

XX OS Synthetic.  
 XX PN EP505908-A1.  
 XX PD 30-SEP-1992.  
 XX PF 18-MAR-1992; 92EP-00104656.  
 XX PR 27-MAR-1991; 91EP-00810220.  
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 XX PI Karjalainen K, Lanzavecchia A, Trautnecker A;  
 XX DR WPI; 1992-325228/40.  
 XX PT DNA encoding chimeric bi-specific polypeptide(s) e.g. CD4 and CD3 binding  
 PT site - for treating HIV infection, and also cancers e.g. ovarian  
 PT carcinoma(s) or leukaemia(s).  
 XX PS Example; Page 10; 19pp; English.  
 XX CC Plasmid pFVCD3-H-gamma-3 comprises a DNA sequence coding for the variable  
 CC regions of the heavy and the light chain (VH and VL) of an anti-human CD3  
 CC antibody (pFVCD3) derived from hybridoma TR66 and for all domains except  
 CC the first of the constant regions of the heavy chain of the human  
 CC immunoglobulin G3. The second strand synthesis of the sequences coding  
 CC for the VL and VH domains of the anti-CD3 hybridoma TR66 was performed by  
 CC T4 DNA polymerase and 5' oligonucleotides 1570 for VH and 1569 for VL  
 CC sequences. Final amplification was then achieved by using the above  
 CC mentioned oligonucleotides and 3' oligonucleotides 1354 and 1239)  
 CC complementary to mouse gamma-HC (immunoglobulin - gamma - heavy chain)  
 CC and C-kappa (constant domain of immunoglobulin kappa-light chain) genes.  
 CC The L region (initiation codon and leader sequence for eukaryotic  
 CC secretion) of the Sp6 HC gene contg. the small intron was amplified by  
 CC using 5' oligonucleotides 1609 and 3' oligonucleotides 1610 which are also  
 CC complementary (20 bp) to oligonucleotides 1570 at its 5' end (ie at the  
 CC beginning of the amplified VH fragment. Junctional and flanking  
 CC oligonucleotides were designed and used to link the L region from Sp6 VH  
 CC and VL fragments together in one 35 PCR reaction: the flanking 5' and 3'  
 CC oligonucleotides were 1609 and 2768 respectively; the latter having  
 CC complementarity to the end for the mouse J-kappa-5 sequence. The  
 CC oligonucleotide 2139 which links VH to VL fragments had 20 bp  
 CC complementarity to the end of the JH2-sequence and to oligonucleotide  
 CC 1569, ie to the 5' end of the VL sequence. Finally, a synthetic piece of  
 CC DNA with SalI compatible ends (oligonucleotides 2119 and 2120)  
 CC corresponding to the linking peptide between VH and VL domains, was  
 CC cloned into a SalI site of the intermediate plasmid to give plasmid  
 CC pFVCD3-H-gamma-3. (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 48 BP; 10 A; 3 C; 24 G; 11 T; 0 U; 0 Other;  
 Query Match 74.0%; Score 14.8; DB 2; Length 48;  
 Best Local Similarity 88.9%; Pred. No. 5.5e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GAGTGGCGGTGGAAGT 19  
 Db 16 GAGTTTCGCTCGAAGTG 33  
 RESULT 10  
 AAQ28730 ID AAQ28730 standard; DNA; 48 BP.  
 XX AC AAQ28730;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 27-FEB-1993 (first entry)  
 XX DE Sequence of oligonucleotide 2120 corresponding to the linking peptide  
 XX between VH and VL domains of plasmid pFVCD3-H-gamma-3.

XX Chimeric polypeptide; cell surface CD4 molecule; HIV type 1; HIV-1;  
 KW human immunodeficiency virus; antigen binding site; cytotoxic T<sup>+</sup> cell;  
 KM CD3 molecule; T-cell receptor complex; PCR; ss.  
 XX  
 OS Synthetic.  
 XX EP505908-A1.  
 XX  
 PD 30-SEP-1992.  
 XX  
 PF 18-MAR-1992; 92EP-00104656.  
 XX  
 PR 27-MAR-1991; 91EP-00810220.  
 XX  
 PA (HOF) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Karjalainen K, Lantavechia A, Trauneker A;  
 XX WPI; 1992-325228/40.  
 XX  
 PT DNA encoding chimeric bi-specific polypeptide(s) e.g. CD4 and CD3 binding  
 PT site - for treating HIV infection, and also cancers e.g. ovarian  
 PT carcinoma(s) or leukaemia(s).  
 XX  
 PS Example; Page 10; 19pp; English.  
 XX  
 CC Plasmid pFvCD3-H-gamma-3 comprises a DNA sequence coding for the variable  
 CC regions of the heavy and the light chain (VH and VL) of an anti-human CD3  
 CC antibody (FvCD3) derived from hybridoma TR66 and for all domains except  
 CC the first of the constant regions of the heavy chain of the human  
 CC immunoglobulin G3. The second strand synthesis of the sequences coding  
 CC for the VL and VH-domains of the anti-CD3 hybridoma TR66 was performed by  
 CC T4 DNA polymerase and 5' oligonucleotides 1570 for VH and 1569 for VL  
 CC sequences. Final amplification was then achieved by using the above  
 CC mentioned oligonucleotides and 3' oligonucleotides 1354 and 1239j  
 CC complementary to mouse gamma-HC (immunoglobulin - gamma - heavy chain)  
 CC and C-kappa (constant domain of immunoglobulin kappa-light chain) genes.  
 CC The L region (initiation codon and leader sequence for eukaryotic  
 CC secretion) of the Sp6 HC gene contg. the small intron was amplified by  
 CC using 5' oligonucleotides 1609 and 3' oligonucleotides 1610 which are also  
 CC complementary (20 bp) to oligonucleotides 1570 at its 5' end (ie at the  
 CC beginning of the amplified VH fragment. Unctional and flanking  
 CC oligonucleotides were designed and used to link the L region from Sp6 VH  
 CC and VL fragments together in one 35 PCR reaction: the flanking 5' and 3'  
 CC oligonucleotides were 1609 and 2768 respectively, the latter having  
 CC complementarity to the end for the mouse J-kappa-5 sequence. The  
 CC oligonucleotide 2139 which links VH to VL fragments had 20 bp  
 CC complementarity to the end of the JH2-sequence and to oligonucleotide  
 CC 1569, ie to the 5' end of the VL sequence. Finally, a synthetic piece of  
 CC DNA with SalI compatible ends (oligonucleotides 2119 and 2120)  
 CC corresponding to the linking peptide between VH and VL domains, was  
 CC cloned into a SalI site of the intermediate plasmid to give plasmid  
 CC pFvCD3-H-gamma-3. (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 SQ Sequence 48 BP; 11 A; 24 C; 3 G; 10 T; 0 U; 0 Other;  
 XX  
 Query Match 74.0%; Score 14.8; DB 2; Length 48;  
 Best Local Similarity 86.9%; Pred. No. 5.5e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GAGGTGCGGTGGAAGTG 19  
 |||||  
 Db 37 GAGGTTCTGTGGAAGTG 20  
 |||||  
 RESULT 11  
 ID ACI86896  
 ACI86896 standard; DNA; 25 BP.  
 XX  
 AC ACI86896;  
 XX  
 DT 14-OCT-2003 (first entry)

XX  
 DS Human microarray DNA oligonucleotide SEQ ID NO 86887.  
 XX  
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; diallelic marker; polymorphism; human;  
 KM cross-species comparison.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003104410-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 15-MAR-2002; 2002US-00098263.  
 XX  
 PR 16-MAR-2001; 2001US-0276759P.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Miltmann MP;  
 XX WPI; 2003-567953/53.  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX  
 PS Claim 1; SEQ ID NO 86887; 9pp; English.  
 XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying diallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 CC  
 XX  
 SQ Sequence 25 BP; 6 A; 5 C; 9 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 72.0%; Score 14.4; DB 9; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 8e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 GTGCGGTGGAAGTGC 20  
 |||||  
 Db 4 GTGCGGTGGAAGTGC 19  
 |||||  
 RESULT 12  
 ID ACHS9512/C  
 ACHS9512 standard; DNA; 25 BP.  
 XX  
 AC ACHS9512;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE DNA target sequence #8648 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;  
 KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 OS Unidentified.  
 XX US2003082596-A1.  
 XX PN 01-MAY-2003.  
 XX PD 08-AUG-2002; 2002US-00215112.  
 XX PF 08-AUG-2001; 2001US-0311040P.  
 XX PR (MITT/) MITTMANN M.  
 XX PA Miltmann M;  
 XX PI WPI; 2003-576608/54.  
 XX DR New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 PT 1  
 XX Claim 1; SEQ ID NO 8648; 9pp; English.  
 XX PS  
 XX CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/psipbidentry.html](http://seqdata.uspto.gov/psipbidentry.html)  
 CC  
 XX SQ Sequence 25 BP; 4 A; 10 C; 6 G; 5 T; 0 U; 0 Other;  
 XX  
 XX Query Match 72.0%; Score 14.4; DB 9; Length 25;  
 XX Best Local Similarity 93.8%; Pred. No. 8e+03; 1; Indels 0; Gaps 0;  
 XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 2 GAGTGCGGGTGAAG 17  
 XX |||||  
 XX DB 24 GAGTGCGGGTGAAG 9  
 XX |||||  
 XX  
 XX RESULT 13  
 XX ABN48299 standard; DNA; 60 BP.  
 XX ID ABN48299;  
 XX AC ABN48299;  
 XX XX 15-JUL-2002 (first entry)  
 XX DT Human spliced transcript detection oligonucleotide SEQ ID NO:21047.  
 XX DE

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX OS Homo sapiens.  
 XX PN WO200210449-A2.  
 XX PD 07-FEB-2002.  
 XX PF 20-JUL-2001; 2001WO-1B001903.  
 XX PR 28-JUL-2000; 2000US-0221607P.  
 XX PR 02-MAY-2001; 2001US-0287724P.  
 XX XX (COMP-) COMPUEN INC.  
 XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX DR WPI; 2002-257383/30.  
 XX DR  
 XX PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 PT 1  
 XX Example 1; SEQ ID NO 21047; 47pp; English.  
 XX PS  
 XX CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridising selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 CC  
 XX SQ Sequence 60 BP; 16 A; 9 C; 24 G; 11 T; 0 U; 0 Other;  
 XX  
 XX Query Match 72.0%; Score 14.4; DB 6; Length 60;  
 XX Best Local Similarity 93.8%; Pred. No. 8.3e+03;  
 XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 3 AGTGCGGGTGAAGT 18  
 XX |||||  
 XX DB 6 AGTGCGGGTGAAGT 21  
 XX |||||  
 XX  
 XX RESULT 14  
 XX ADJ23951/C standard; DNA; 20 BP.  
 XX ID ADJ23951;  
 XX AC ADJ23951;  
 XX XX 20-MAY-2004 (first entry)  
 XX DT Human endothelial lipase antisense oligonucleotide, SEQ ID 2349.  
 XX DE

```
KM Antilipemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KM Human; Endothelial lipase; dyslipidaemia; high density lipoprotein; HDL;
KM Cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
PN MO2004009541-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022410.
XX
PR 19-JUL-2002; 2002US-0397106P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Bhat BG;
XX
PI high density lipoprotein or cardiovascular disorders.
XX
DR WPI; 2004-132912/13.
XX
PT New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX
PS Claim 3; SEQ ID NO 2349; 1007bp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
XX
Query Match 71.0%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 TGAGTGGCGGTGGAAGTG 19
DB 19 TGAGATTGGGAGGAGTG 1
XX
RESULT 15
ADJ23488/c
ID ADJ23488 standard; DNA; 20 BP.
XX
AC ADJ23488;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 1886.
XX
KM Antilipemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KM Human; Endothelial lipase; dyslipidaemia; high density lipoprotein; HDL;
KM Cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
```

```
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
PN MO2004009541-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022410.
XX
PR 19-JUL-2002; 2002US-0397106P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Bhat BG;
XX
PI high density lipoprotein or cardiovascular disorders.
XX
DR WPI; 2004-132912/13.
XX
PT New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX
PS Claim 3; SEQ ID NO 1886; 1007bp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
XX
Query Match 71.0%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 TGAGTGGCGGTGGAAGTG 19
DB 20 TGAGATTGGGAGGAGTG 2
XX
Search completed: December 24, 2005, 12:29:02
Job time : 173.4 secs
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